

# **EXHIBIT 11**



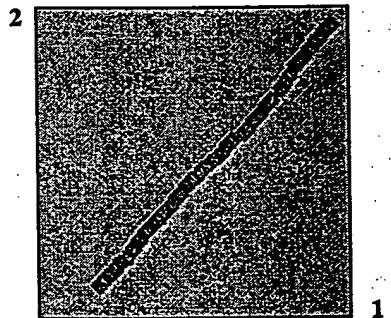
## Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix **BLOSUM62**, gap open: **11**, gap extension: **1**  
x\_dropoff: **50**, expect: **10.0**, wordsize: **3**, Filter  Alignmt

Sequence 1 lcl|seq\_1 Length 955 (1..955) PMPE PTA 2462

Sequence 2 lcl|seq\_2 Length 839 (1..839) POMP90B



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 162 bits (411), Expect = 2e-38  
Identities = 208/781 (26%), Positives = 329/781 (41%), Gaps = 114/781 (14%)

Query: 179 TFFVSEHQSCFLFMDNICKIQINTAGKGAIYA-GTSNSFESENCCDFFINNACCGAGAIF 237  
TF+ + CF DNI T TA GAI G + + LF + A C G  
Sbjct: 85 TPLGNGYTLCP---DNI---TTTASNPAGAINVQQGKTLGISGFSLF--SCAYCPPGTG 136

Query: 238 SPICSLTGND----RGNIVFYNNRCFKNVETASSEASDGGAIKVTTRLDVT---GNGRRI 289  
GN ++VF+ KN TA +GGAI+ D N +  
Sbjct: 137 YGAIQTKGNNTLKDNLSSLVFH----KNCSTA----EGGAIQCKGSSDAELKIENNQNL 186

Query: 290 FFSDNITKNYGGAIYAPVVTLVDNGPTYFINNVANN---KGGAIYI-DGTSNSKISADR 344  
PS+N + + GGAIYA +T+V GPT F NN +N KGGAI I D + ++AD  
Sbjct: 187 VFSSENSSTSKGAIYADKLTIVSGGPTLFSNNNSVNGSSPKGAIISKDSSGECLSTADL 246

Query: 345 HAIIFNENITVNNTSANGTSTSANPPRNAITVASSGEILLGAGSSQNLIFYDPIEVSN 404  
I F+ N + + + T T RN-I + + LA + FYDPI  
Sbjct: 247 GDITFDGKIIKTSGGSSTVT----RNSIDLGTGK-FTKLRAKDGFGIFFYDPITGGG 299

Query: 405 AG-VSVSFNKEADQTGSVVFSGATVNSAD-FHQRNLTQTKTPAPLTLSNGFLCIEDHAQLT 462  
+ + + + + D TG +VFSG ++ + NL + P+TLS G L ++D +T  
Sbjct: 300 SDELNINKKETVDTYGKIVFSGEKLSDEEKARAENLASTFNQPITLSAGSLVLDGVSVT 359

Query: 463 VNRFTQ-TGGVVSILNGAVLSCYKNGAGNSASNASITLKHIGLNLSILKSGAEIPLLWV 521  
+ TQ G V + G L +G +ITL ++ +N++S+ G  
Sbjct: 360 AKQVTQEAGSTVMDLGTQTPSSG----GETITLTLDINIASLGGGG----T 407

Query: 522 EPTMNSNNYTADTAATPSSLSDVVLKSLIDDYGNSPYESTDLTHALSSQPMISISEASDNQL 581  
P + N TA A T + ++L+D GN+ YE L +S+P + I ++  
Sbjct: 408 SPAKLATN-TASQAITIN---AVNLVDADGNA-YEDPILA---TSKPFTAIVATTNAST 458

Query: 582 RSDDMDFSGLNVP--HYGWQGLWSWGAKTQDPEPASSATITDPKKANRFHRTLLLWLP 639  
+ D VP HYG+QG W+ W D E A+ +T LTW  
Sbjct: 459 VTQPTDNLNTYVPPTHGYQGNWTVTW----DTETAT-----KTATLTWEQ 500

Query: 640 AGYVPSPKHRSPLIANTLWG--NMLLATESLKNSAELTPSDHFWGITGGGLGMVYQEP 697  
GY P+P+ + PL+ NTLWG + L A ++L + + H G GL +++  
Sbjct: 501 TGYSNPERQGPLVPNTLWGAFSDLRAIQNLMDISVNGADYHR--GFWVSGLANFLHKSG 558

Query: 698 RENHPGPHMRSSGYFAGMIA--GQTHTFSLKFSQTYTKLNE-RYAKN--NVSSKNYSCQG 752

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using [BLAST](#) engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  blastp  Matrix  PEGSUM62

Parameters used in [BLASTN](#) program only:

Reward for a match:  Penalty for a mismatch:

Use [Mega BLAST](#) Strand option  Not Applicable

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter  Align

Sequence 1 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
DYGNNSPYESTDLTHALSSQPMILS1SEASDNYLRSIDDMUFSGLNVPHYGWQGLWSWGWARU  
DPEPASSATITDPKKANRFHRTLLLTLWPAGYVPSPKHRSPLIANTLWGNMLLATESLKN  
AELTSDHPFWGTTGGGLGMMVYQEPRENHGPFHMRSSGYFAGMIAGQTHTPSLKFSQTYT  
KLNERYAKNNVSSKNYSCQGEMLFSLQEGPLLAKLVGLYSGYGDHNCHHFYTQGENLTSQGT  
FRSQTMGGAVFFDLPMPKPGGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV  
LVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS  
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGETALRF.
```

Sequence 2 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
IT'INAVNLVDALGNAEYEDP'LATSKPFTAIATVATTAATVIAQPTLNLTINIVPFPHYGIQGN  
WTVTWDTEATKATLTLWEQTGYSPNPERQGPLVPNTLWGAFSDLRAIQNLDISVNGAD  
YHRGFVWSGLANLHKSGSDTKRKFHRNSAGVALGVYAKTPSDDIFSAFCOLFGKD  
LVSKNNANIYAGSLYYQHISYWSAWQNLLQNTIGAEAPLVNAQLTYCHASNDMKTNT  
TYAPRKTTYAEIKGDWGNDCPFGVELGATVPIQTESSLLFDMSPPFLKFQLVTHQDDFKE  
NNSDQGRYFESSNLTNLSPIGIKPERFANNDTASYHVTAAASPDI  
VRSNPDCCTSLLVS  
PDSAVWVTKANNLARSAMQLQAGNLYSLSHNIEIFSQFGFELRGSSRTYNVDLGSKIQF
```

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)

+ F S+GY G+ A FS F Q + K + +KN N+ + + Q  
 Sbjct: 559 SDTKRKFRHNSAGYALGVYAKTPSDDIFSAFCQQLFGKDKDYLVSKNNANIYAGSLYYQH 618

Query: 753 EMLPSLQEGFLLAALKLVGLYSYGDHN-----CHHFYTQGENLTS-----OGTFR 795  
 +S + LL +G + N CH N+T+ +G +  
 Sbjct: 619 ISYWSAWQN-LLQNTIGAEAPLVLNAQLTYCHASNDMKTNMTTYAPRKTTYAEIKGDWG 677

Query: 796 SQTMGGAVFFDLPMPKGSTHI-LTAPFLGALGIYSSLSHFTEVGAYPRSFSTKPLINV 854  
 + G + +P++ S + +PFL +++ F E + + + L N+  
 Sbjct: 678 NDCFGVELGATVPIQTESSLLFDMDYSPFLKFQLVHTHQDDPKENNSDQGRYFESSNLTNL 737

Query: 855 LVPIGVKGSFMNATQRQPQAWTVELAYQPVLVYRQELEIATQLLAS--KGIWFGSGSPSSRH 912  
 +PIG+K A + + V AY P + R + T LL S +W + +R  
 Sbjct: 738 SLPIGKPERF-ANNDTASYHVTAAAYS DIVRSNPDCTSLLVSPDSAVWVTKANNLARS 796

Query: 913 A 913  
 A  
 Sbjct: 797 A 797

CPU time: 0.22 user secs. 0.03 sys. secs. 0.25 total secs.

Lambda K H  
 0.316 0.132 0.396

Gapped  
 Lambda K H  
 0.267 0.0410 0.140

Matrix: BLOSUM62  
 Gap Penalties: Existence: 11, Extension: 1  
 Number of Hits to DB: 9570  
 Number of Sequences: 0  
 Number of extensions: 806  
 Number of successful extensions: 12  
 Number of sequences better than 10.0: 1  
 Number of HSP's better than 10.0 without gapping: 1  
 Number of HSP's successfully gapped in prelim test: 0  
 Number of HSP's that attempted gapping in prelim test: 0  
 Number of HSP's gapped (non-prelim): 2  
 length of query: 955  
 length of database: 326,887,585  
 effective HSP length: 133  
 effective length of query: 822  
 effective length of database: 281,363,015  
 effective search space: 231280398330  
 effective search space used: 231280398330  
 T: 9  
 A: 40  
 X1: 16 ( 7.3 bits)  
 X2: 129 (49.7 bits)  
 X3: 129 (49.7 bits)  
 S1: 41 (21.6 bits)  
 S2: 78 (34.7 bits)

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)  
**Reference:** Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  blastp  Matrix  BLOSUM62

Parameters used in **BLASTN** program only:

Reward for a match:  Penalty for a mismatch:

Use Mega BLAST Strand option  Not Applicable

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter   Align

Sequence 1 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
DIYGNSTPYESTDULITHALSSQPMILSISSEASUNQLRSDDMDFSGLNVPHYGWQGLWSWGWAQTQ  
DPEPASATITDPKKANRFHRTLLLTLWPAGYVPSPKHRSPLIANTLWGNMLLATESLKN  
AELTPSDHPFWGITCGGLGMVMVQEPRHENPGFHMRSGGYFAGMLAGQTHTFSLKFQSQTYT  
KLNERYAKNNVSSRNYSQCGEMLFSLQEGFLLAKLVGLYSYGDHNCHHFYTQGENLTSQGT  
FRSQTMGGAVFDLPMKPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPINV  
LVPIGVKGSFMNATQRPOAWTVELAYQPVLRYRQELEIATQLLASKGIWFSGSPSSRHAMS  
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
HYGYQGINWIVIWKQGSSAQEKTTATLTIWEQTYGSPNPERQGSLVFNTLWGSFSDIKATQNL  
MDISVNGADYHRGFVWSGLGNFLHKSGSDTKRKFRHNSAGYALGVYAAQTPSEDVFSAAFC  
QLFGKDQDYLVSKNSSTVYAGSIYYQHISYWNWTNTLLQNTLGAEAPLVNAQLAYCHAS  
NNMKTNMTDTYAPPKTTYSEIKGDDWGNDCFGVEFGAKAPIETASLLFDMDYSPFVKLQLVH  
AHQDDDFKENNSDQGRYFESNLTNLSPMFIGVKLEKPSSHDTASYNLAYAPDIVRSNP  
CTASLLVSPTSAVWVTKANNLARHAFLQAGNYLALTRNTLEFSQFGFELRGSCRTYNID  
LGSKIQF
```

Align

Clear Input

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



## Blast 2 Sequences results

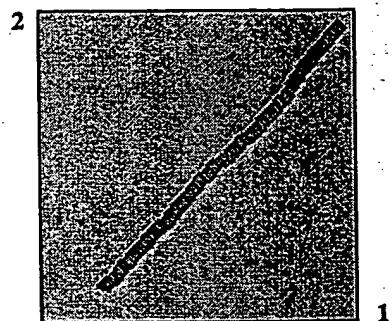
### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix **BLOSUM62**, gap open: **11**, gap extension: **1**

x\_dropoff: **50**, expect: **10.0**, wordsize: **3**, Filter  Aligner

Sequence 1 lcl|seq\_1 Length 955 (1 .. 955) PMPE PTA 2462

Sequence 2 lcl|seq\_2 Length 847 (1 .. 847) POMP 91 A



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 174 bits (441), Expect = 7e-42  
Identities = 196/767 (25%), Positives = 318/767 (40%), Gaps = 101/767 (13%)

Query: 190 LFMGNICIQTNACKGGAIYAGTSNSFESNNCDLFFINNACCAAGGAFSPICSLTGN--- 246  
Sbjct: 97 LCFDNIT--TQSSHGAISVSGTNKTLISGFSLF--SCAYCPPGATGYGAIKAVGNTTI 152

Query: 247 --RGNIVFYNNRCKNVTASSEASDGGAAIKVTTRLDVTGNRGRIFFSNDNITKNYGGAIY 304  
Sbjct: 153 KDNSSLVFH----KNCSTGEGGAIQCKASSSEAEKIENNQNLF-AENSSSSSGGAIY 206

Query: 305 APVVTLVDNGPTYFINN---VANNKGGAIIYI-DGTSNSKISADRHAIIFNENIVNTSA 360  
Sbjct: 207 ADKLTIVSGGPTLFSNNVSASSPKGAICIKDGGECSLTADLGDTFDGNKIIKTNGG 266

Query: 361 NGTSTSANPPRRNAITVASSGEILLGAGSSQNLIFYDPIEVSNAGVSFSNKE--ADQT 418  
Sbjct: 267 SPTVT-----RNSIDLGSQSKFTKLNAKEFGIFGYDPI-TGGGSDELNINKQDTVDYT 319

Query: 419 GSUVFSGATVNSADFQ-QRNLQTKTPAPLTLNSNGFLCIEDHAQLTVNRFTQT-GGVVSLG 476  
Sbjct: 320 GKIVFSGERLSDEEKVAANLKSDFKQPLKIGSGSLILKDGVTLETKSFTQTEGATVMD 379

Query: 477 NGAVLSCYKNGAGNSASNASITLKHIGLNLSILKSGAEIPLLWVEPTNNNSNNYTADAA 536  
Sbjct: 380 LGTTLQTPSSGG-----ETITLTNLDINVASLGGGGVAPDPAKVEATTESKTVTINA-- 431

Query: 537 TFSLSDVKVLSLIDDYGNPSYESTDLTHALSSQPMLSIS--EASDNQLRSDDMDFSGLNVP 594  
Sbjct: 432 -----VNLVDDNGNA-YEYPILA--ASQPFTAIEVRSGSSGSITKPTTNLENYTPP 479

Query: 595 -HYGWQGLWSWGAKTQDPPEPASSATITDPKKANRFHRTLLLWLPAGYVPSPKHRSPLI 653  
Sbjct: 480 THYGYQGNWTWTWKQ-----GSSAQ-----EKTATLTWEQTGYSPNPERQGSLV 523

Query: 654 ANTLWGNMILLATESLKNSAELTPSDHPFW-GITGGGLGMMVYQEPRRENHPGFHMRSRGYF 712  
Sbjct: 524 FNTLWGS-FSDIRAIQNLMDISVNGADYHRGFVWVSGLGNFLHKSGSDTKRKFRHNSAGYA 582

Query: 713 AGMIA--GQTHTFSLKFQSQTYTKLNERVAKNNVSSKNYSCQGEMLF-----SLQE 760

G+ A FS F Q + K ++ Y + SS Y+ G + + +L +  
 Sbjct: 583 LGVYAQTPSEDVFSAAFCQLFGK-DKDYLVSNSSTVYA--GSIYYQHISYWNTWNTLLQ 639

Query: 761 GFLLAALKVGLYSYGDHNCHHFYTQGENLTS-----QGTFRSQTMGGAVFFDLP 808  
 L A+ + + CH N+T +G + + G P

Sbjct: 640 NTLGAEAPLVLAQLAYCHASNMMKTNMTDTYAPPKTTYSEIKGDWGNDCPGVEFGARAP 699

Query: 809 MKPFGSTHILTAFLGALGISSLSHFTEVGAYPRSFSTKPLINVLVPIGVKGSMNAT 868  
 ++ + +PF+ +++ F E + + L N+ +PIGVK +

Sbjct: 700 IETASLLFDMDMYSFVKLQLVHAHQDDFKENNDSQGRYFESENLLTNLSMPIGVKLEKF-SH 758

Query: 869 QRPOQAWTVELAYQPVLRYRQELEIATQLLAS--KGIWFSGSGSPSRHA 913

+ + + LAY P + R + LL S +W + +RHA

Sbjct: 759 KDTASYNLTLAYAPDITVRSNPCTASLLVSPTSAVWVTKANNLARHA 805

CPU time: 0.23 user secs. 0.03 sys. secs 0.26 total secs.

Lambda K H  
 0.316 0.132 0.396

Gapped Lambda K H  
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 10,082

Number of Sequences: 0

Number of extensions: 843

Number of successful extensions: 16

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 955

length of database: 326,887,585

effective HSP length: 133

effective length of query: 822

effective length of database: 281,363,015

effective search space: 231280398330

effective search space used: 231280398330

T: 9

A: 40

X1: 16 ( 7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.6 bits)

S2: 78 (34.7 bits)

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site  
**Reference:** Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program **blastp** Matrix **DEUTSCHM62**

Parameters used in **BLASTN** program only:

Reward for a match:  Penalty for a mismatch:

Use Mega BLAST Strand option **Not Applicable**

Open gap **11** and extension gap **1** penalties

gap x\_dropoff **50** expect **10.0** word size **3** Filter  Align

Sequence 1 Enter accession or GI **clone e** or download from file

or sequence in FASTA format from: **0** to: **0**

```
DYGNSPYESTDLTHALSSQPMILS1SEASDUNQLRSULMDFSGLNVPHYGWQJGLNSWGWAQTV
DPEPASSATITDPKKANRFHRTLLLTLWPAGYVPSPKHRSPLIANTLWGNMLLATESLKN
AEELPSDHPFWGTGGGLGMMVVQEPRENHGPFHMRSSGYFAGMIAGQHTPSLKFSQTYT
KLNERYAKNVNSKKNYSCQGEMLFSLQEGFLLAKLVLGGLYSGDHNCCHHFYTQGENLTSQGT
FRSQTMGGAVFFDLPMPKGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV
LVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQELEIAHQLLASKGTIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI **pomp91b** or download from file

or sequence in FASTA format from: **0** to: **0**

```
DISVNGADYSRGFWVWSLLANFLINKSGSDTRKAFAHMMSAGYALGVYAQTFSDDVCSAARCV
LFGKDKDYFVSKNSSTIYAGSIYYQHISYWNTWNFLLQNTLGAEAPLVLNQLTYCHASN
NMKTNMTNTYTPKVNTPSEIKGDWGNDCFGVVEFKAKAPIETASLLFDMDYSPFVQLQLVHA
HQDDFKENNNSDQGRYFESNNLTNL SMPIGVKLEKF SHKD TASYNLTLAYAPDIVRSNPDC
TASILLVSPTSAVWVTKANNLARHAFILOQAGNYLALT RNTTELF SQFGFELRGSCR TYNIDL
GSKIQF
```

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



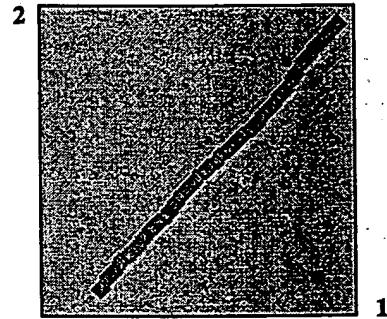
## Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix **BLOSUM62**, gap open: **11**, gap extension: **1**  
 x\_dropoff: **50**, expect: **10.0**, wordsize: **3**, Filter  Align

Sequence 1 lcl|seq\_1 Length 955 (1..955) PMPETPTA 244Z

Sequence 2 lcl|seq\_2 Length 846 (1..846) POMP91B



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 162 bits (409), Expect = 4e-38  
 Identities = 193/790 (24%), Positives = 324/790 (40%), Gaps = 101/790 (12%)



Query: 172 GAI STANTFVVSENQSCFLMDN---IC---IQTN TACKGGAIYAGTSNSPFESNNCDLFF 225  
 G S N SE F+ N +C I T ++ G +GT+ + + + LF

Sbjct: 68 GKDSPLNKSCFSETTENLSFIGNGYTLCFDNITTQSSHGAISVSGTNKTLDISGFSLFS 127

Query: 226 INNACCAG---GAIFSPICSLTGNGRNIVFYNNRCFKNVETASSEASDGGAIKVTRLD 281  
 C G GAI + + + ++VE+ KN TA A + T L

Sbjct: 128 CAYCCPPGTTGYGAIQTKGTTLKDNNSSLVFH----KNCSTAEGGAIQCKSSSSTAELK 182

Query: 282 VTGNRGRIFFSDNITKNYGGAIYAPVVTLVDNGPTYFINN-VANN---KGGAIYI-DGTS 336  
 + N+ +F S+N +K GGAIYA +T+V GPT F NN V++N KGGAI I D

Sbjct: 183 LENNKNLVF-SENSKEKGAIYADKLTI VSGGPTLFNNNSVSHNSPKGGAIKIDS 241

Query: 337 NSKISADRHAIIIFNENIVTNVTSANGTSTSANPPRRNAITVASSSGEILLGAGSSQNLIF 396  
 ++A+ I F+ N + + T T RN+I + S LA + F

Sbjct: 242 ECSLTANLGDI TDGKNIITNGGSPTVT-----RNSIDLGSGGKFTKLNKEFGFI 295

Query: 397 YDPIEVSNAGVSFSFNK---EADQTGSVVFSGATVNSAD-FHQRLQTKTPAPLTLNGF 452  
 YDPI + + NK + TG +VFSG ++ + NL++ PL + G

Sbjct: 296 YDPIANTGGSTEIELNKTESDTTYTGKIVFSGEKLSDEEKTV PANLKS YFKQPLKIGAGS 355

Query: 453 LCIEDHAQLTVNRFTQT-GGVVSLGNGAVLSCYKNGAGNSASNASITLKHIGLNLSILK 511  
 L ++D L + TQT G V + G L S+S +ITL ++ +N++S+

Sbjct: 356 LVLKDGVTL EAKKITQTKGSTVMDLGTQ-----PSSSGETITLTNLDINIASLGG 409

Query: 512 SGAEIPLLWVEPTNNNNYTAFTAFTFSLSDVKLSSLIDYGNSPYESTDLTHLSSQML 571  
 G P A A+ ++S ++L++ N+ YE L+ + S +

Sbjct: 410 GGGTAPA-----KLATNTASQAISIAAVNLVNTDSNT-YEDPILSASKSFAIT 457

Query: 572 SISEASDNQLRSDDMDFSGLNVP-HYGWQGLWSWGAWKTQDPPEPASSATITDPKKANRFH 630  
 ++ S + + + + P HYG+QG W+ W + SSA

Sbjct: 458 ATT--SSSTVTPPETNLKNYTPPHTHYGYQGNWTVTW-----KQGSSAQ-----E 499

Query: 631 RTLLLTLWPAGYVPSPKHRSPLIANTLWNGLMILATESLKNSAELTPSDHPF-WGITGGGL 689  
 +T LTW GY P+P+ L+ NTLWG T +++N +++ + + G L

Sbjct: 500 KTATLTWEQTGYSPNPERVGSVPNTLWG-AFSDTRAIQNLM DISVNGADYSRGFWVSSL 558

Query: 690 GMMVYQEPRENHPGFHMRSSGYFAGMIA--GQTHTPSLKFSQTYTKLNERAYAKNNVSSKN 747

+ + + F S+GY G+ A S F Q + K + + N SS  
 Sbjct: 559 ANFLNKSGSDTKRKFRHHSAGYALGVYAQTPSDDVCSAACFQLFGKDKDYFVSKN-SSTI 617

Query: 748 YSCQGEMLF-----SLOEGFLLAKLVGLYSYGDHNCHHFYTQGENLTS----- 790  
 Y+ G + + +L + L A+ + + CH N+T+  
 Sbjct: 618 YA-GSIYYQHISYWNNTWNTLQLGAEAPLVLNQLTYCHASNNMKTNMTNTYTPKNV 675

Query: 791 ----QGTFRSQTMGAVFPDLMKPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSF 845  
 +G + + G P++ + +PF+ +++ FE + +  
 Sbjct: 676 TPSEIKGDWGNDCFGVEFGAKAPIETASLLFDMSPFVKLQLVHAHQDDFKENNNSDQGRY 735

Query: 846 STKTPLINVLVPIGVKGGSFMNATQRQPQAWTVELAYQPVLYRQELEIATQLLAS--KGIWF 903  
 L N+ +PIGVK + + ++ LAY P + R + LL S +W  
 Sbjct: 736 FESNNLTNLSPMIGVKLEKP-SHKDTASYNLTLAYAPDIVRSNPDCTASLLVSPTSAVWW 794

Query: 904 GSGSPSSRHA 913  
 + +RHA  
 Sbjct: 795 TKANNLARHA 804

CPU time: 0.23 user secs. 0.03 sys. secs 0.26 total secs.

Lambda K H  
 0.316 0.132 0.396

Gapped  
 Lambda K H  
 0.267 0.0410 0.140

Matrix: BLOSUM62  
 Gap Penalties: Existence: 11, Extension: 1  
 Number of Hits to DB: 10,170  
 Number of Sequences: 0  
 Number of extensions: 837  
 Number of successful extensions: 13  
 Number of sequences better than 10.0: 1  
 Number of HSP's better than 10.0 without gapping: 1  
 Number of HSP's successfully gapped in prelim test: 0  
 Number of HSP's that attempted gapping in prelim test: 0  
 Number of HSP's gapped (non-prelim): 2  
 length of query: 955  
 length of database: 326,887,585  
 effective HSP length: 133  
 effective length of query: 822  
 effective length of database: 281,363,015  
 effective search space: 231280398330  
 effective search space used: 231280398330  
 T: 9  
 A: 40  
 X1: 16 ( 7.3 bits)  
 X2: 129 (49.7 bits)  
 X3: 129 (49.7 bits)  
 S1: 41 (21.6 bits)  
 S2: 78 (34.7 bits)